

Ref ID: A01

TITLE Genetic test for equine severe combined immunodeficiency disease  
JOURNAL Patent: US 5976803-A 26 02-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..243  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 15; DB 6; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTAATGTTGCTCT 15  
141 TTTAATGTTGCTCT 127

RESULT 2  
AR083113/c 248 bp DNA linear PAT 01-SEP-2000  
LOCUS AR083113  
DEFINITION Sequence 27 from patent US 5976803.  
ACCESSION AR083113  
VERSION AR083113.1 GI:10009903  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 248)  
AUTHORS Meek, K.D.  
TITLE Genetic test for equine severe combined immunodeficiency disease  
JOURNAL Patent: US 5976803-A 27 02-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..248  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 15; DB 6; Length 248;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTAATGTTGCTCT 15  
146 TTTAATGTTGCTCT 132

RESULT 3  
HUMADH7CIV 539 bp DNA linear PRI 07-MAR-1996  
LOCUS HUMADH7CIV  
DEFINITION Homo sapiens class IV alcohol dehydrogenase 7 (ADH7) gene, 5' flanking region.  
ACCESSION L39009  
VERSION L39009.1 GI:625123  
KEYWORDS ADH7 gene; alcohol dehydrogenase; alcohol dehydrogenase IV.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 539)  
AUTHORS Yokoyama, H., Baraona, E. and Lieber, C.S.  
TITLE Upstream structure of human ADH7 gene and the organ distribution of its expression  
JOURNAL Biochem. Biophys. Res. Commun. 216 (1), 216-222 (1995)  
PUBMED 7488092  
COMMENT Original source text: Homo sapiens DNA.  
FEATURES Location/Qualifiers  
source 1..539  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="4q23-24"  
/cell\_type="fibroblast"  
/tissue\_type="forebrain"  
complement(1..539)  
/gene="ADH7"  
1..539  
/note="G00-362-911"  
5'UTR 1..539  
/note="G00-362-911"

gene  
mRNA  
5'UTR

Query Match 100.0%; Score 15; DB 8; Length 539;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTAATGTTGCTCT 15  
338 TTTAATGTTGCTCT 352

RESULT 4  
BV274862/c 638 bp DNA linear STS 25-JAN-2005  
LOCUS BV274862  
DEFINITION S232P6460RD5.T0 Beagle Canis familiaris STS genomic sequence tagged site.  
ACCESSION BV274862  
VERSION BV274862.1 GI:57437091  
KEYWORDS STS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 638)  
AUTHORS Lindblad-Toh, K.  
TITLE The genome sequence of Canis familiaris  
JOURNAL Unpublished (2004)  
COMMENT Contact: Kerstin Lindblad-Toh  
Whitehead Institute for Biomedical Research, Center for Genome Research  
320 Charles Street, Cambridge, MA 02141, USA  
Tel: 6172521477

870 ID NO: 2

CDS 135..2332  
/gene="Pnc401"  
/codon\_start=1  
/product="leaf protein"  
/protein\_id="BA25906.1"  
/db\_xref="GI:3107905"  
/translation="MGCEKKAIVRNKKKTGVSQISASPTMESHLHGNAHVS  
TVSTPTQVVRCTACGNDGCQVTRSTYKMLKTLIERGKQEVHSITGLEGHNP  
LVYTYTVAALTLQKRFKSIPLAKVBNQGRPSIFNPMINAFCSGNVEAMKI  
FKRMKEGCKPTASTFNALIKGFCIIGKEEESKLEIMRESENIKPDRTYNIIVQA  
MCNKNIEKAMGVHRWAGLAKPDVYTYNTIARVARGKETSRAELISOMONKVA  
PVRTCGIIVDGYSKEGMMADALAKFTYKMGCGVHPRLIFNSLAKGFLDITDKVD  
ETLTMGEFVAKPDVYTYSTTNAMSSAGLMEKEWFDWIKSGIBDNHAFSLAK  
GVRAKGEKKAELALEAMATGAPVNVPTTIIISGCSAAKKEBALVYDRKCRMD  
QPNLTFTETLIMGCEANEPMKAEELIQIMEEMVGLPRKNTVQLVADAMRAIGFINA  
KRIINDQSSVLIPRTDERPVEDLQRYOCEKINGSYKTLPPDNDKRPITLANKVENRE  
DNVHRGDHHEQIMKSPFSLPEMTGSIITINONGSFTLASOTTKSKSRATISNMNA  
AKAILISNCGFKPNPLVYIOPRLVQIGIRHYINSCLVLA"

ORIGIN  
Query Match 100.0%; Score 13; DB 15; Length 2332;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACATCAAC 13  
|||||  
Db 1711 TGTACATCAAC 1723

RESULT 82  
LOCUS D85101 2343 bp mRNA linear PLN 02-MAY-1998  
DEFINITION Phorbilis nil Pnc401 mRNA for leaf protein, complete cds.  
ACCESSION D85101  
VERSION D85101.1 GI:3107904  
KEYWORDS Pnc401; leaf protein.  
SOURCE Ipomoea nil (Japanese morning glory)  
ORGANISM Ipomoea nil  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Convolvulaceae; Ipomoeae; Ipomoea.  
1 (sites)  
REFERENCE  
AUTHORS Sage-Ono, K., Ono, M., Harada, H. and Kamada, H.  
TITLE Accumulation of a clock-regulated transcript during  
JOURNAL flower-inductive darkness in phorbilis nil  
PUBMED 9536066  
2 (bases 1 to 2343)  
REFERENCE  
AUTHORS Sage-Ono, K.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAY-1996) Kimiyo Sage-Ono, University of Tsukuba,  
Institute of Biological Science, Tennoudai 1-1-1, Tsukuba, Ibaraki  
305, Japan (E-mail:kimiyo@sakura.cc.tsukuba.ac.jp,  
Tel:0298-53-6588, Fax:0298-53-6006)  
FEATURES  
source Location/Qualifiers  
1..2343  
/organism="Ipomoea nil"  
/mol\_type="mRNA"  
/cultivar="Violet"  
/sub\_species="Choisy"  
/db\_xref="taxon:35883"  
/tissue\_type="cotyledon"  
/clone\_lib="lambda gtl0"  
/dev\_stage="young seedling"  
1..2343  
/gene="Pnc401"

CDS 135..2332  
/gene="Pnc401"  
/codon\_start=1  
/product="leaf protein"  
/protein\_id="BA25906.1"  
/db\_xref="GI:3107905"  
/translation="MGCEKKAIVRNKKKTGVSQISASPTMESHLHGNAHVS  
TVSTPTQVVRCTACGNDGCQVTRSTYKMLKTLIERGKQEVHSITGLEGHNP  
LVYTYTVAALTLQKRFKSIPLAKVBNQGRPSIFNPMINAFCSGNVEAMKI  
FKRMKEGCKPTASTFNALIKGFCIIGKEEESKLEIMRESENIKPDRTYNIIVQA  
MCNKNIEKAMGVHRWAGLAKPDVYTYNTIARVARGKETSRAELISOMONKVA  
PVRTCGIIVDGYSKEGMMADALAKFTYKMGCGVHPRLIFNSLAKGFLDITDKVD  
ETLTMGEFVAKPDVYTYSTTNAMSSAGLMEKEWFDWIKSGIBDNHAFSLAK  
GVRAKGEKKAELALEAMATGAPVNVPTTIIISGCSAAKKEBALVYDRKCRMD  
QPNLTFTETLIMGCEANEPMKAEELIQIMEEMVGLPRKNTVQLVADAMRAIGFINA  
KRIINDQSSVLIPRTDERPVEDLQRYOCEKINGSYKTLPPDNDKRPITLANKVENRE  
DNVHRGDHHEQIMKSPFSLPEMTGSIITINONGSFTLASOTTKSKSRATISNMNA  
AKAILISNCGFKPNPLVYIOPRLVQIGIRHYINSCLVLA"

ORIGIN  
Query Match 100.0%; Score 13; DB 15; Length 2343;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTACATCAAC 13  
|||||  
Db 866 TGTACATCAAC 878

RESULT 83  
LOCUS AY057573 2393 bp mRNA linear PLN 07-OCT-2001  
DEFINITION Arabidopsis thaliana AT3953700/F4P12\_400 mRNA, complete cds.  
ACCESSION AY057573  
VERSION AY057573.1 GI:15982930  
KEYWORDS FLI\_CDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 2393)  
REFERENCE  
AUTHORS Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,  
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,  
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,  
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,  
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,  
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,  
Toriuchi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,  
Davis, R.W., Theologis, A. and Ecker, J.R.  
TITLE Arabidopsis cDNA clones  
JOURNAL Unpublished  
2 (bases 1 to 2393)  
REFERENCE  
AUTHORS Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,

SEQ ID NO: 3

misc\_feature 488..496  
/note="poc. glycosylation site"  
misc\_feature 506..514  
/note="poc. glycosylation site"  
intron 542..1442  
/number=4  
repeat\_region 882..1069  
/note="Alu repetitive sequence"  
exon 1443..1535  
/number=5  
intron 1536..1788  
/number=5  
exon 1789..1879  
/number=6  
intron 1880..2736  
/number=6  
exon 2737..2928  
/note="additional exon 6B (used in 1441, omitted in 1431)"  
repeat\_region 2796..2928  
/note="sequence homologous to the repetitive element in  
thyroglobulin (Tyr)"  
misc\_feature 2877..2885  
/note="poc. glycosylation site"  
misc\_feature 2919..2927  
/note="poc. glycosylation site"  
intron 2929..3302  
/note="6b"  
exon 3303..3365  
/number=7  
intron 3366..3594  
/note="intron VII"  
exon 3595..4113  
/number=8  
polyA\_signal 4074..4079  
/note="putative"  
ORIGIN  
Query Match 100.0%; Score 14; DB 9; Length 4113;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAATAAGGAGAT 14  
Db 1395 AAATAAGGAGAT 1382

RESULT 28  
SSU30500 4402 bp mRNA linear VRL 01-SEP-1995  
LOCUS  
DEFINITION sicilian gandfly fever virus glycoprotein precursor polypeptide  
ACCESSION U30500  
VERSION U30500.1 GI:973314  
KEYWORDS  
SOURCE Sandfly fever sicilian virus  
ORGANISM Sandfly fever sicilian virus  
VIRUSES; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus;

unclassified Phlebovirus.  
REFERENCE 1 (bases 1 to 4402)  
AUTHORS Glass, P.J. and Parker, M.D.  
TITLE Direct Submision  
JOURNAL Submitted (28-JUN-1995) Pamela J. Glass, Virology, USAMRIID, Bldg 1425, Ft. Detrick, Frederick, MD 21702, USA  
FEATURES  
source  
1..4402  
/organism="Sandfly fever sicilian virus"  
/mol\_type="mRNA"  
/db\_xref="taxon:28292"  
19..4044  
/codon\_start=1  
/product="glycoprotein precursor polypeptide"  
/protein\_id="AA75043.1"  
/db\_xref="GI:973315"  
/translation="MFEITLLIVLATFLIVGNTLSEKMNLSLTSTCPSTGPG  
IIEKYNQEPMAKMGPDHCHRPBEGDPKRTHERNAKKQIKYTTAPPTKFGSGDET  
KSLGSLTNDGNNMGPAIIYCDTDFIRNITGEOSPVDYERLKNNAEKDATTQ  
RTKTEMEVRAVLDSNQIAHHEIQKENEIQKNDLRDAIKQGEHESMKLRVES  
DARVGLKEELKQLYKIFPDQATKDELQHAKEWOSLRKIKDEPESIPQAKSSNS  
VLTMTTAVLSLSSMAAPAGMNAATHINNRGLKFPALITGTEDEHCKKIDYGV  
TCSRPHLKSIDRYPPNSHYHRLALBHNDNYIKVSTISCTETFRNAECSKIR  
KLAIVCRGVSGVITADSGEIGIYCKENESLMEKCIQCRKVRKPKQGLIQLD  
MVCQNSTDYTGPKQVLKGYCKIGMDYRHCHEFASMEVPPALFKKQGLYDMSR  
IRKNDVLEKENFICYAKENADDSNHGAKSVYTECKNDVPSQNRKICSGNTPCS  
KFAACHELPEVCEVAPGAGPIEYVGGVGIQPMGLYERAMVLEAMPPEVTSBPTC  
DSQCECLDSHILVSTGPMISGAVCSGACASITVPESTEIMTPYGAASISGDI  
GIHLSHDEVOVSSHTRVHCEPKDCVAHSCVLCABGIIINQCHTLASAFVYTLVLA  
VLMPLIVLRKCLVFRVAPALVLPFSWIVKLAFTSRKLSITERTIARINBEICMR  
PEGAAARHRDRDRIPRSAYVLAIIILISVSACSDDTKIASIKYICVAKGSKSV  
CTISGLINVAAGPIGSECTVTLKGPDSAKREKITIYASIELICSGQSVTQCYVE  
CISRRRCGVAECKGDAQRMNSTVUSREPQITNNSVISENRCIEQCGYGCACRV  
YASCLFPHARLRATKRAIKVFNCIDMSHRLVLEITDPNKEKVSMTGMTTPFSWG  
SMTLADPBGITGTNSYSFLSSSGTFLSVDENASMEBRGFLGSIKSSSAAALTAH  
KSCVAPDIIIRYKPMTDIVDCSTSLIDPFAVFLGALPQTRNKTFSSSIDKTIQAF  
TSGIYHASMISLSEFDFEERVSCLASPVNITGCGSCNBEARVCOAANQNTTL  
HYHTLDSNLTIWMDVLSPKSTDCRVVHLSLTPQVMDVYSCQGYKAMSIAGTLVAMN  
PDDRHRHEETNSVYVNPRTGRMDSSMASGLVDMGLCPRTAGVILGTITLAIIVPLIM  
LVLCVPLVGMIRPALLRKL"  
ORIGIN  
Query Match 100.0%; Score 14; DB 13; Length 4402;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAATAAGGAGAT 14  
Db 4168 AAATAAGGAGAT 4181

RESULT 29  
HSM807414/c 4703 bp mRNA linear PRI 30-AUG-2003  
LOCUS  
DEFINITION Homo sapiens mRNA; cDNA DKFZp686f2193 (from clone DKFZp686f2193).  
ACCESSION BX647270  
VERSION BX647270.1 GI:34366298

Seq ID NO: 4

Db 24 TCTTTGAGCACAGAT 38

RESULT 3

AA080645

LOCUS AA080645 266 bp mRNA linear EST 28-OCT-1997

DEFINITION EST100 Sugarcane leaf roll Saccharum sp. cDNA clone B80-rev similar to coded for by C. elegans cDNA, mRNA sequence.

ACCESSION AA080645

VERSION AA080645.1 GI:1620362

KEYWORDS EST.

SOURCE Saccharum sp.

ORGANISM Saccharum sp.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE 1 (bases 1 to 266)

AUTHORS Carson, D.L. and Botha, F.C. E

TITLE Sugarcane cDNA from leaf roll tissue

JOURNAL Unpublished (1996)

COMMENT Contact: Deborah Lee Carson

Biotechnology

South African Sugar Association Experiment Station

Private Bag X02, Mount Edgecombe, 4300, South Africa

Tel: 2731593205

Fax: 2731595406

Email: biotech@sugar.org.za

Partial sequence of a 500 bp clone

Seq primer: M13 Reverse.

FEATURES Location/Qualifiers

source

1..266

/organism="Saccharum sp."

/mol\_type="mRNA"

/db\_xref="taxon:15819"

/clone="B80-rev" E

/tissue\_type="leaf roll"

/clone\_lib="Sugarcane leaf roll"

/note="Vector: Lambda ZAP II; Site\_1: EcoRI; mRNA was prepared from the leaf roll of the commercial sugarcane variety Nco 376. cDNA was synthesised using standard protocols and ligated to an annealed amplification adaptor set. cDNA was then PCR amplified. Amplified cDNA was ligated and cloned into the Eco RI site of the Lambda ZAP II phage vector." E

ORIGIN

Query Match 100.0%; Score 15; DB 1; Length 266;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTTTGAGCACAGAT 15

|||||

Db 106 TCTTTGAGCACAGAT 120

RESULT 4

DN955667/c

820 ID NO:5

```
/translation="SPPLSHHTLPNQQPTVTLSRRSSSHEETPGSHPLVGHGECKWP
GCETLSDGQGIKHLNTEHALDDNSTAQCVRQVQVQVQLEIQAKESERLQAMWAHL
HMRSEKFPQPLNPNPVGSSFSKVTYSAADSPDGLVHPPTSAAPVTPPLRPGGLG
SASLHGCGPARRSDDKFCSPISSELAQNHEFYKNADVRPFTYASLIROAILLETPDR
QLTNELYNMFTRMFAVFRNTATWKNVVRHNLKHCFCVRVENVKGAVTVDEREYQ
KRRPKMTSGPTLVKNMISGLSYGALNASYQAALASSPFLNSPGMLNFGSASSLLP
LSHDVGAPVEPLPSNGSSSPLTLPLPFLCSPQLPFLARLSPRRPTS"
misc_feature
597..815
/feature="FOXp4"
/feature="FH; Region: FORKHEAD"
/db_xref="CDD:smart00339"

ORIGIN

Query Match      100.0%; Score 14; DB 8; Length 1279;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAAGCAGTGAC 14
|||||
Db 517 GGAGAAGCAGTGAC 530

RESULT 42
MUSBMP5M
LOCUS      MUSBMP5M      1359 bp      mRNA      linear      ROD 01-APR-1995
DEFINITION Mus musculus bone morphogenetic protein 5 (BMP5) mRNA, complete cds.
ACCESSION L41145
VERSION L41145.1 GI:755033
KEYWORDS bone morphogenetic protein 5.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 1359)
AUTHORS King, J.A., Marker, P.C., Seung, K.J. and Kingsley, D.M.
TITLE BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
JOURNAL Dev. Biol. 166 (1), 112-122 (1994)
PUBMED 7958439
COMMENT Original source text: Mus musculus (strain C3H/Kw) CDNA to mRNA.
FEATURES
    source
        1..1359
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C3H/Kw"
            /db_xref="taxon:10090"
        1..1359
            /gene="BMP5"
        <1..>1359
            /gene="BMP5"
        1..1359
            /gene="BMP5"
        /codon_start=1
        /product="bone morphogenetic protein 5"
        /protein_id="AAA64612.1"
```

```
/db_xref="GI:755034"
/translation="MHMTVFLRLGIVFLWSQVGVYKAGKGLGNHVVHSFIYRLRL
NHERRETOEILSLGLHPRPSPCKOASSAPFLMLDIYNAMSEDNPEEYLVRVS
LAGAKETRGVDPASNGYVHRLHLPRTPLTQTOSPLASLHDTNFLADAMWMSFVN
LVERDKDFSHQRHVKERFPLQIQIPIHGEANTAAEFRIYKDKGNHRFENETIKISIYQ
IKEYTRDADLFLDTRTKQALDVGVLVDFTVTSNNHVINPNQNLGLQICAPTGDG
RSINVKAGLIVRGHGPQKFPFVAFKASEVLLRSVRAASKRKNQNKNSHODPS
RMP5AGDYNTEQKACKKHELTVSFRDLGQMDMIIAPEGYAAFCDCGCSFFLNAMH
NATNHAIVQTLVHLNMFDPKVPCCAPTCLNAISLVLYDDSSNVILKKYRMVVRSCG
CH"

ORIGIN

Query Match      100.0%; Score 14; DB 9; Length 1359;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAAGCAGTGAC 14
|||||
Db 562 GGAGAAGCAGTGAC 575

RESULT 43
BC061764/c
LOCUS      BC061764      1413 bp      mRNA      linear      ROD 12-NOV-2003
DEFINITION Rattus norvegicus protein kinase inhibitor p58, mRNA (cdna clone IMAGE:5621087), partial cds.
ACCESSION BC061764
VERSION BC061764.1 GI:38197557
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE
1 (bases 1 to 1413)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buétow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udgin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
```

Seq ID NO:6

/db\_xref="taxon:7242"

ORIGIN

Query Match 100.0%; Score 14; DB 6; Length 2963;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATTGTCCTATG 14  
|||||

Db 855 ACATTGTCCTATG 842  
|||||

RESULT 19  
XLU17249 3562 bp mRNA linear VRT 27-SEP-1995  
LOCUS  
DEFINITION Xenopus laevis gastric H(+)-K(+)-ATPase alpha-subunit mRNA,  
complete cds.

ACCESSION  
VERSION U17249.1 GI:596055  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus laevis (African clawed frog)

REFERENCE  
AUTHORS Mathews,P.M., Claeys,D., Jaissner,F., Geering,K., Horisberger,J.D.,  
Kraehenbuhl,J.P. and Rossier,B.C.  
TITLE Primary structure and functional expression of the mouse and frog  
alpha-subunit of the gastric H(+)-K(+)-ATPase  
JOURNAL Am. J. Physiol. 268 (5 Pt 1), C1207-C1214 (1995)  
PUBMED 7762614  
REFERENCE 2 (bases 1 to 3562)  
AUTHORS Mathews,P.M.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-1994) Paul M. Mathews, Institute of Pharmacology  
and Toxicology, University of Lausanne, Rue du Bugnon 27, CH-1005,  
Lausanne, Switzerland

FEATURES  
source  
1..3562  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/sex="female"  
/cell\_type="parietal cell"  
/tissue\_type="stomach mucosa"  
/dev\_stage="adult"  
31..3126  
/codon\_start=1  
/product="gastric H(+)-K(+)-ATPase alpha-subunit"  
/protein\_id="AAA76601.1"  
/db\_xref="GI:596056"  
/translation="MGKKEQDMYSVENEREGDGMVDVKKKASKKKKESNKK  
EMDINHEITVEELQKYYTSVSKGLKSAFAAEVILRDGPNELKPPKTPYIKFARQ  
LAGLQCLMVAAVICLIAFGTEESQGLTSADNLAIITLIVVVVTCGCGYQEFK  
STNIIASFNLVPOQATVVRDQKFIINQLVVDLVEIKGDRVPADIRIITSQGC  
KVDNSSLGTESEPQTRSPYTHESPLETRNIAFFSTMCLEGTATGTLIINTGRTTIIGR

Qy 1 ACATTGTCCTATG 14  
|||||

Db 3210 ACATTGTCCTATG 3223  
|||||

RESULT 20  
AC006119/c  
LOCUS  
DEFINITION Mus musculus clone UMGC:mbac10gap from 14D1-D2 (T-Cell Receptor  
Alpha Locus), complete sequence.

ACCESSION AC006119  
VERSION AC006119.1 GI:3962517  
KEYWORDS HTG.  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,  
Magness,C.L., Green,P., Olson,M.V. and Hood,L.  
TITLE Large-Scale Sequence Analysis of the Mouse T-Cell Receptor Alpha  
Locus  
JOURNAL Unpublished (1998)  
REMARK University of Washington Human Genome Center  
Box 352145 Seattle, WA 98195  
Contact: Inyoul Lee (borah@u.washington.edu)  
2 (bases 1 to 5207)  
Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,  
Magness,C.L., Green,P., Olson,M.V. and Hood,L.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Human Genome Center, University of  
Washington, Box 352145, Seattle, WA 98195, USA  
Overlapping Sequences:  
5': UMGC:mbac37 (Genbank Accession: AC005402)  
3': UMGC:mbac92 (Genbank Accession: AC005855)

Qy 1 ACATTGTCCTATG 14  
|||||

Db 3210 ACATTGTCCTATG 3223  
|||||

Query Match 100.0%; Score 14; DB 5; Length 3562;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATTGTCCTATG 14  
|||||

Db 3210 ACATTGTCCTATG 3223  
|||||

RESULT 20  
AC006119/c  
LOCUS  
DEFINITION Mus musculus clone UMGC:mbac10gap from 14D1-D2 (T-Cell Receptor  
Alpha Locus), complete sequence.

ACCESSION AC006119  
VERSION AC006119.1 GI:3962517  
KEYWORDS HTG.  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,  
Magness,C.L., Green,P., Olson,M.V. and Hood,L.  
TITLE Large-Scale Sequence Analysis of the Mouse T-Cell Receptor Alpha  
Locus  
JOURNAL Unpublished (1998)  
REMARK University of Washington Human Genome Center  
Box 352145 Seattle, WA 98195  
Contact: Inyoul Lee (borah@u.washington.edu)  
2 (bases 1 to 5207)  
Lee,I.Y., Wang,K., Smit,A.F., Yu,J., Wong,G.K.-S., Iadonato,S.P.,  
Magness,C.L., Green,P., Olson,M.V. and Hood,L.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Human Genome Center, University of  
Washington, Box 352145, Seattle, WA 98195, USA  
Overlapping Sequences:  
5': UMGC:mbac37 (Genbank Accession: AC005402)  
3': UMGC:mbac92 (Genbank Accession: AC005855)

Seq ID NO: 7

JOURNAL COMMENT  
Unpublished (2005)  
Contact: William Gregory  
Nematode Genomics, University of Edinburgh  
ICAPB  
Ashworth Laboratories, King's Buildings, Edinburgh, EH9 3JT  
Tel: +44 131 650 7317  
Email: b.gregory@ed.ac.uk  
The library was constructed in pSPORT1 vector (Invitrogen) using  
Generacer (Invitrogen) 5' capped adult female mRNA by William  
Gregory, University of Edinburgh. Sequencing was performed by PSU,  
Sanger Centre, Cambridge, UK.  
Plate: 19 row: e column: 01  
Seq primer: T7(TAATACGACTCACTATAGG)  
High quality sequence stop: 241.  
FEATURES  
source  
1..282  
/organism="Litomosoides sigmodontis"  
/mol\_type="mRNA"  
/db\_xref="taxon:42156"  
/clone="Lg afl\_19e01"  
/sex="Female"  
/clone\_lib="Litomosoides sigmodontis adult female 1 (high  
molecular weight)"  
ORIGIN  
Query Match 100.0%; Score 15; DB 8; Length 282;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCATCTAGATCAATT 15  
|||||  
Db 217 GCATCTAGATCAATT 203  
RESULT 3  
AA906249  
LOCUS AA906249 385 bp mRNA linear EST 19-MAY-1998  
DEFINITION OJ93gl2.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1505926 3' similar to contains L1.t3 L1 repetitive element ;  
mRNA sequence.  
ACCESSION AA906249  
VERSION AA906249.1 GI:3041372  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 385)  
AUTHORS NCIC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-@email.nih.gov  
This clone is available royalty-free through LLML; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Insert Length: 830 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 367.  
FEATURES  
source  
1..385  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1505926"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI-CGAP-CCBI) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "  
ORIGIN  
Query Match 100.0%; Score 15; DB 1; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCATCTAGATCAATT 15  
|||||  
Db 266 GCATCTAGATCAATT 280  
RESULT 4  
B83992/c  
LOCUS B83992 400 bp DNA linear GSS 09-APR-1999  
DEFINITION RPC111-21H8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-21H8,  
genomic survey sequence.  
ACCESSION B83992  
VERSION B83992.1 GI:2925124  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 400)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and  
Venter,J.C.  
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Other\_GSSs: RPC111-21H8.TP  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research